

Design Technique for Use in Engineering of Deamidation Rates of Peptides, Proteins, Hormones, and Peptide-Like, Protein-Like and Hormone-Like Molecules

Abstract

A method that quantitatively explains the primary sequence dependence of deamidation has been invented on the basis of a simple steric and catalytic model. Application of this method to the known deamidation rates of peptides has produced a table of coefficients that permits prediction of primary sequence deamidation rates and provides that ability to engineer amides with specific rates. This work permits a better understanding of deamidation, provides a prediction procedure for protein engineering, and will allow improved computation of peptide and protein primary, secondary, and tertiary structure deamidation rates. Not only can this method be used for engineering amides, but it should also work for isomerization and racemization of carboxylic acids.